



RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 09/718,321
Source: OIP
Date Processed by STIC: 5/21/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002

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OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/718,321

DATE: 05/21/2002
 TIME: 14:28:49

Input Set : A:\Cura-99.app
 Output Set: N:\CRF3\05212002\I718321.raw

**Does Not Comply
 Corrected Diskette Needed**

4 <110> APPLICANT: Shimkets, Richard A.
 5 Leach, Martin D.
 7 <120> TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS
 AND METHODS OF
 8 USE THEREOF
 10 <130> FILE REFERENCE: 15966-599
 12 <140> CURRENT APPLICATION NUMBER: US/09/718,321
 12 <141> CURRENT FILING DATE: 2002-05-07
 12 <150> PRIOR APPLICATION NUMBER: 60/163,783
 13 <151> PRIOR FILING DATE: 1999-11-24
 15 <160> NUMBER OF SEQ ID NOS: 1468
 17 <170> SOFTWARE: CuraGen Patent Formatter Version 0.9

ERRORED SEQUENCES

23675 <210> SEQ ID NO: 1405
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 23677 <212> TYPE: PRT
 23678 <213> ORGANISM: Homo sapiens
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 23767 <223> OTHER INFORMATION: cSNP translation
 23769 <400> SEQUENCE: 1411
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10 delete

DO NOT use a template.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/718,321

DATE: 05/21/2002
TIME: 14:28:55

Input Set : A:\Cura-99.app
Output Set: N:\CRF3\05212002\I718321.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/718,321

DATE: 05/21/2002

TIME: 14:28:55

Input Set : A:\Cura-99.app

Output Set: N:\CRF3\05212002\I718321.raw

L:659 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35
L:676 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:693 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:37
L:710 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:38
L:2177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120 after pos.:0
L:23687 M:252 E: No. of Seq. differs, <211> LENGTH:Input:12 Found:11 SEQ:1405
L:23771 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1411